

1 ATGATTACAATAGTTTATTAATCCTAGCCTATCTGCTGGGTTCCATTCTGGTCTGGATTGGACAAGTATCTTTCAAATCAATCTACGGAGC 100
TACTAATGTTATCAAAATAATTAGGATCGGATAGACGACCAAGCTAAGGTAGACCAGAGACCTAACCTGTTTATAAGAAAGTTTAGTTAGATCGGCTCG

1 M I T I V L L I L A Y L L G S I P S G L W I G Q V F F Q I N L R E H 34

101 ATGGTTCTGGTAAACACTGGAACGACCAACACCTTCGCAATTTTAGGTAAGAAAGCTGGTATGGCAACCTTTGTGATTGACTTTTTCAAAGGAACCCCTAGC 200
TACCAAGACCATTGTGACCTTGTCTGTTGTGAAGGCGTAAATCCATTCTTTCCACCATACCGTTGGAAACACTAACTGAAATAAGTTTCTCTGGGATCG

35 G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A 67

201 AACGCTGCTCCGATTATTTTTCATCTACAAAGGCGTTTCTCCTCTCATCTTTGGACTTTTGGCTGTTATCGGCCATACCTTCCCTATCTTTGCGAGGATTT 300
TTGCGACGAGGCTAATAAAAAAGTAGATGTTCCGCAAGAGGAGAGTAGAATCCTGAAACCGACAATAGCCGGTATGGAAGGATAGAAACGTCCTTAA

68 T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F 100

301 AAAGGTGGTAAGGCTGTCCCAACCAAGTCTGGAGTGATTTTCGGATTTCGGCTATCTTCTGTCTACCTTGGCTATCTTCTTTGGAGCTCTCTATC 400
TTTCCACCATTCCGACAGCGTTGGTACCGACCTCACTAAAAGCTAAACGGGATAGAACGAGATGGAACGCTAATAGAAACCTCGAGAGATAG

101 K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L 134

401 TTGGCAGTATGATTTCACTGTCTAGTGTACAGCATCGATTGCGGCTGTTATCGGGTTCTGCTCTTCCACTTTTGGTTTATCCTGAGTAACCTATGA 500
AACCGTCATACTAAAGTGACAGATCACAGTGTGCTAGCTAACCGGACAATAGCCCAAGACGAGAAAGGTGAAACCAAAATAGGACTCATTTGATCT

135 G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D 167

501 CTCTCTTTCATCGCTATTATCTTAGCACTTGTAGTTGATTATCATTCGTCAAGGACAAATATAGCTCGTATCAAAATAAACTGAAATTTGGTC 600
GAGAGAGAGTAGCGATAATAGAAATCGTGAACGATCAAACTAATAGTAGCAGTATTCCTGTTATATCGAGCATAGTTTATTTTGTACTTTTAAACCAG

168 S L F I A I I L A L A S L I I I R H K D N I A R I K N K T E N L V 200

601 CCTTGGGGATTGAACCTAACCCATCAAGATCCTAAAAATAA 642 SEQ ID NO:2
GGAACCCCTAACTGGATTGGGTAGTCTAGGATTTTATT SEQ ID NO:11

201 P W G L N L T H Q D P K K • 213 SEQ ID NO:1

FIG. 1

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1	A T G A T T A C A A T A G T T T T A T T A A T C C T A G C C T A T C T G C T G G G T T C G A T T C C A T C T G G T C T G G A T T G G A C A A G T A T T C T T T C A A T C A A T C T A C G C G A G C	100
	T A C T A A T G T T A T C A A A A T A A T T A G G A T C G G A T A G A C G A C C A A G C T A A G G T A G A C C A G A G A C C T A A C C T G T T C A T A A G A A A G T T T A G T T A G A T G C G C T C G	
1	I M I T I V L L I L A Y L L I L A Y L L G S I P S G L W I G Q V F F Q I N L R E H	34
101	A T G G T T C T G G T A A C A C T G G A A C G A C C A C A C C T T C G C A T T T T A G G T A A G A A A G C T G T A T G G C A A C C T T T G T G A T T G A C T T T T C A A A G G A A C C C T A G C	200
	T A C C A A G A C C A T T G T G A C C T T G C T G G T T G T G A A G C G T A A A T C C A T T C T T T C G A C C A T A C C G T T G G A A C A C T A A C T G A A A A A G T T T C C T T G G G A T C G	
35	G S G N T G T T N T F R I L G K K A G M A T F V I D F F K G T L A	67
201	A A C G C T G C T T C C G A T T A T T T T C A T C T A C A A G G C G T T T C C T C T C A T C T T T G G A C T T T T G G C T G T T A T C G G C C A T A C C T T C C C T A T C T T T G C A G G A T T T	300
	T T G C G A C G A A G G C T A A T A A A A G T A G A T G T T C C G C A A A G A G A G A G A T A G A A C C T G A A A C C G A C A A T A G C C G G T A T G G A A G G G A T A G A A A C G T C C T A A A	
68	T L L P I I F H L Q G V S P L I F G L L A V I G H T F P I F A G F	100
301	A A A G G T G G T A A G G C T G T C G C A A C C A G T G C T G G A G T G A T T T C G G A T T T G C G C C T A T C T T C T G T C T A C C T T G C G A T T A T C T T C T T T G G A G C T C T C T A T C	400
	T T T C C A C C A T T C C G A C A G C G T T G G T C A G A C C T C A T A A A G C C T A A A C C G G A T A G A A G A C A G A G A T G G A A C G C T A A T A G A A G A A A C C T C G A G A G A T A G	
101	K G G K A V A T S A G V I F G F A P I F C L Y L A I I F F G A L Y L	134
401	T T G G C A G T A T G A T T T C A C T G T C A G T G T C A C A G C A T C G A T T G C G G C T G T T A T C G G G T T C G C T C T T T C C A C T T T T T G G T T T A T C C T G A G T A A C T A T G A	500
	A A C C G T C A T A C T A A A G T A C A G A T C A C A G T G T C G T A G C T A A C G C C G A C A A T A G C C C A A G A C G A G A A G G T G A A A A A C C A A A A T A G G A C T C A T T G A T A C T	
135	G S M I S L S S V T A S I A A V I G V L L F P L F G F I L S N Y D	167
501	C T C T C T T C A T C G C T A T T A T C T T A G C A C T T G C T A G T T T G A T T A T C A T T C G T C A T A A G A C A A T A T A G C T C G T A T C A A A A A T A A A A C T G A A A A T T T T G G T C	600
	G A G A G A A A G T A G C G A T A A T A G A A T C G T G A A C G A T C A A A C T A A T A G T A A G C A G T A T T C C T G T T A T A T C G A G C A T A G T T T T A T T T T G A C T T T T A A A C C A G	

SEQ ID NO:2

SEQ ID NO:11

213 SEQ ID NO:1

FIG. 1